Please amend the application as follows to comply with requirements for patent applications containing nucleotide sequence and/or amino acid sequence disclosures in adherence with rules 37 C.F.R. § 1.821-1.825:

IN THE SPECIFICATION:

Please replace the paragraph beginning at page 8, line 6, with the following rewritten paragraph:

–As should be understood, the list of transcription factors is known to the artisan. The members of each class and subclass are specifically incorporated by reference. Binding sites for transcription factors are well known in the art. A database of transcription factors is available though TRANSFAC - The Transcription Factor Database at http://transfac.gbf.de/TRANSFAC/. Preferred transcription factors include NF-κB, ETS, STAT, p53, Ap-1 family, steroid hormone and related families. In a preferred embodiment, NF-κB binding sites are used. A variety of sites can be used including the consensus site 5'GGGRNYYYCC3' (SEQ ID NO:1) described in Chen and Ghosh, Oncogene 1999, 18:6845-6852. –

Please replace the paragraph beginning at page 12, line 6, with the following rewritten paragraph:

– Each pool is assayed for the ability to activate a transcription factor-dependent reporter in a transient transfection assay in tissue culture cells. Pools with the desired regulatory activity (either stimulatory or inhibitory) are further subdivided and screened until a single cDNA is isolated with the desired activity. As a control, positive pools are screened for the ability to regulate a mutant version of the reporter, in which the NF-κB binding sites have been mutated. Positive pools which do not regulate the mutant reporter are determined to be specific. In a preferred

embodiment, the NF-κB-responsive promoter has two copies of the κB site (5'-GGGGACTTTCC-3' (SEQ ID NO 2)). The mutant reporter is identical except that the two NF-κB sites have been mutated to (5'-ATCCACTTTCC-3' (SEQ ID NO:3)). Eventually, a single cDNA is obtained which will encode a gene product that can regulate the activity of the transcription factor of study. This individual clone is then sequenced to identify the cDNA it contains and the gene product it expresses.–

Please replace the paragraph beginning at page 19, line 8, with the following rewritten paragraph:

– 293T cells were maintained in DME supplemented with 10% fetal calf serum, 100 U/ml of penicillin and streptomycin, and 2mM glutamine in humidified 5% CO_2 at 37°C. Cells were plated at 9 x 10^4/well in 24-well dishes 24 hr before transfection by the calcium phosphate method. A total of 372 ng of DNA was transfected, including 2 ng of pCSK-LacZ, 20 ng of the Igκ$_2$-IFN-LUC reporter, and 350 ng of pool DNA. The Igκ$_2$-IFN-LUC reporter contains two copies of the Igκ$_2$ κB site (5'-GGGGACTTTCC-3' (SEQ ID NO:2)) upstream of the interferon-β minimal reporter (-55 to +19) driving luciferase expression (Fujita, T. et al., Cell 49:357-67 (1987)). pCSK-lacZ vector constitutively expresses β–galactosidase and is unaffected by NF-κB activity.–

Please replace the paragraph beginning at page 20, line 16, with the following rewritten paragraph:

– For efficient and economical expression screening, a reporter assay for NF-κB activation that is quantitative and highly sensitive was employed. In this assay, pool DNA was transiently transfected into 293T cells with the Igκ$_2$-IFN-LUC reporter, which contains two copies of the Igκ κB site (5'-GGGGACTTTCC-3' (SEQ ID NO:2)) upstream of the interferon-β minimal promoter (-55 to +19) (Fujita, T., et al., *Cell* 49:357-67 (1987)) driving luciferase expression. For normalization for transfection efficiency and extract recovery, the transfection includes the pCSK-

lacZ vector (Condie, B.G., et al., *Mol Cell Biol* 10:3376-85 (1990)) which constitutively expresses β-galactosidase and is unaffected by NF-κB activity. To maximize the number of cDNAs that could be assayed in a transfection, the complexity was determined (number of cDNAs per pool) which would allow reliable detection of a single active clone in a mixture of cDNAs. Pilot experiments using TRAF2, an adapter protein in the TNFα pathway (Rothe, M., et al., *Science* 269:1424-7 (1995)), suggested that a pool complexity of 100 cDNAs would allow detection of molecules possessing 3-fold lower specific activity than TRAF2 in this assay (data not shown). The sensitivity of detection of luciferase and β-galactosidase activities allowed us to scale down the size of the transfection and to minimize the amount of pool DNA required.–

Please replace the paragraph beginning at page 21, line 7, with the following rewritten paragraph:

– Three secondary screens were applied. First, the NF-κB dependence of a pool's activity was tested by comparing its fold induction on the Igκ$_2$-IFN-LUC reporter to that on the MUT-IFN-LUC reporter, which contains mutations in the Igκ κB motifs (5'-ATCCACTTTCC-3' (SEQ ID NO:3)). Second, the specific activities which might function upstream of the IKK complex were tested by assessing their activity in the presence of the IKKβ K44A kinase-dead dominant negative. Third, each κB-specific positive pool was tested in the presence of kinase dead TBK1 (K38A), an IKK-related kinase which we recently identified (Pomerantz, J.L. & D. Baltimore, *Embo J* 18:6694-704 (1999)) (see also (Tojima, Y., et al., *Nature* 404:778-82 (2000))). Examples of these secondary screens are shown in FIG. 2. Of the 41 positive pools, 34 were found to be dependent on the κB sites for activity. Each of these specific pools was found to be inhibited by cotransfection with the IKKβ K44A, and one pool (pool 178) was also inhibited by cotransfection with TBK1 K38A (FIG. 2).–